

From Amendment

FIGURE 1: ISS-pST gene construct

1 GCTAGCATGG CCCTGTGGAT GCGCCTCCTG CCCCTGCTGG CGCTGCTGGC
5 51 CCTCTGGGGA CCTGACCCAG CCGCAGCCCT CGAGATGTTT CCAGCTATGC
101 CACTTTCTTC TCTGTTCGCT AACGCTGTTC TTCGGGCCCA GCACCTGCAC
151 CAACTGGCTG CCGACACCTA CAAGGAGTTT GAGCGCGCCT ACATCCCGGA
201 GGGACAGAGG TACTCCATCC AGAACGCCCA GGCTGCCTTC TGCTTCTCGG
251 AGACCATCCC GGCCCCACG GGCAAGGACG AGGCCAGCA GAGATCGGAC
10 301 GTGGAGCTGC TGCCTTCTC GCTGCTGCTC ATCCAGTCGT GGCTCGGGCC
351 CGTGCACTTC CTCAGCAGGG TCTTACCAA CAGCCTGGTG TTTGGCACCT
401 CAGACCGCGT CTACGAGAAG CTGAAGGACC TGGAGGAGGG CATCCAGGCC
451 CTGATGCGGG AGCTGGAGGA TGGCAGCCCC CGGGCAGGAC AGATCCTCAA
501 GCAAACCTAC GACAAATTTG ACACAACTT GCGCAGTGAT GACGCGCTGC
15 551 TTAAGAACTA CGGGCTGCTC TCCTGCTTCA AGAAGGACCT GCACAAGGCT
601 GAGACATACC TGCGGGTCAT GAAGTGTCGC CGCTTCGTGG AGAGCAGCTG
651 TGCCTTCTAG TCTAGA (SEQ ID NO: 4)

20 ATG...GCC- insulin secretory signal.

GCTAGC- *Nhe* I restriction site incorporated into construct in order to ligate into plasmid.

CTCGAG- *Xho* I restriction site incorporated into construct in order to ligate secretory signal and pST.

25 TCTAGA- *Xba* I restriction site incorporated into construct in order to ligate into plasmid.

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FIGURE 2: ISS-pST peptide sequence.

1 MALWMRLPL LALLALWGPD PAAALEMFPA MPLSSLFANA VLRAQHLHQL
5 51 AADTYKEFER AYIPEGQRYG IQNAQAFCF SETIPPTGK DEAQQRSDVE
101 LLRFSLLLIQ SWLGPVQFLS RVFTNSLVFG TSDRVYEKLK DLEEGIQALM
151 RELEDGSPRA GQILKQTYDK FDTNLRSDDA LLKNYGLLSC FKKDLHKAET
201 YLRVMKCRRE VESSCAF (SEQ ID NO:3)

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MAL.....AAA- insulin secretory signal, cleaved upon secretion of pST.

LE- function of XhoI cleavage site; result in no predicted secondary structural changes to pST.